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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/600,158

DATE: 08/04/2004

TIME: 11:03:09

Input Set : N:\Crif3\RULE60\10600158.raw

Output Set: N:\CRF4\08042004\J600158.raw

1 <110> APPLICANT: Wang, Xin Wei
 2 Harris, Curtis C.
 3 Fornace Jr., Albert J.
 4 Coursen, Jill D.
 5 Zhan, Qimin
 6 The Government of the United States of America
 7 as represented by the Secretary of the
 8 Department of Health and Human Services
 9 <120> TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
 10 Polypeptide Activity, and Inhibitors of Such Activity
 11 <130> FILE REFERENCE: 015280-367100US
 12 <140> CURRENT APPLICATION NUMBER: US/10/600,158
 13 <141> CURRENT FILING DATE: 2003-06-20
 14 <150> PRIOR APPLICATION NUMBER: US/09/534,811
 15 <151> PRIOR FILING DATE: 2000-03-24
 16 <150> PRIOR APPLICATION NUMBER: US 60/126,069
 17 <151> PRIOR FILING DATE: 1999-03-25
 18 <160> NUMBER OF SEQ ID NOS: 32
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1343
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (284)..(781)
 28 <223> OTHER INFORMATION: human growth arrest and DNA-damage-inducible
 29 protein (GADD45)
 30 <400> SEQUENCE: 1
 31 ggcagtggct gggaggcagc ggcccaatta gtgtcgtgcg gcccggtggcg aggcgaggtc 60
 32 cggggagcga gcgagcaagc aaggcgggag ggggtggccgg agctgcggcg gctggcacag 120
 33 gaggaggagc ccgggcgggc gaggggcggc cggagagcgc cagggcctga gctgccggag 180
 34 cggcgcctgt gagtgagtgc agaaagcagg cgcccgcgcg ctagccgtgg caggagcagc 240
 35 ccgcacgcgc cgctctctcc ctgggcgacc tgcagtttgc aat atg act ttg gag 295
 36 Met Thr Leu Glu
 37 1
 38 gaa ttc tcg gct gga gag cag aag acc gaa agg atg gat aag gtg ggg 343
 39 Glu Phe Ser Ala Gly Glu Gln Lys Thr Glu Arg Met Asp Lys Val Gly
 40 5 10 15 20
 41 gat gcc ctg gag gaa gtg ctc agc aaa gcc ctg agt cag cgc acg atc 391
 42 Asp Ala Leu Glu Glu Val Leu Ser Lys Ala Leu Ser Gln Arg Thr Ile
 43 25 30 35
 44 act gtc ggg gtg tac gaa gcg gcc aag ctg ctc aac gtc gac ccc gat 439

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45   Thr Val Gly Val Tyr Glu Ala Ala Lys Leu Leu Asn Val Asp Pro Asp
46               40               45               50
47   aac gtg gtg ttg tgc ctg ctg gcg gcg gac gag gac gac gac aga gat   487
48   Asn Val Val Leu Cys Leu Leu Ala Ala Asp Glu Asp Asp Arg Asp
49               55               60               65
50   gtg gct ctg cag atc cac ttc acc ctg atc cag gcg ttt tgc tgc gag   535
51   Val Ala Leu Gln Ile His Phe Thr Leu Ile Gln Ala Phe Cys Cys Glu
52               70               75               80
53   aac gac atc aac atc ctg cgc gtc agc aac ccg ggc cgg ctg gcg gag   583
54   Asn Asp Ile Asn Ile Leu Arg Val Ser Asn Pro Gly Arg Leu Ala Glu
55               85               90               95               100
56   ctc ctg ctc ttg gag acc gac gct ggc ccc gcg gcg agc gag ggc gcc   631
57   Leu Leu Leu Leu Glu Thr Asp Ala Gly Pro Ala Ala Ser Glu Gly Ala
58               105               110               115
59   gag cag ccc ccg gac ctg cac tgc gtg ctg gtg acg aat cca cat tca   679
60   Glu Gln Pro Pro Asp Leu His Cys Val Leu Val Thr Asn Pro His Ser
61               120               125               130
62   tct caa tgg aag gat cct gcc tta agt caa ctt att tgt ttt tgc cgg   727
63   Ser Gln Trp Lys Asp Pro Ala Leu Ser Gln Leu Ile Cys Phe Cys Arg
64               135               140               145
65   gaa agt cgc tac atg gat caa tgg gtt cca gtg att aat ctc cct gaa   775
66   Glu Ser Arg Tyr Met Asp Gln Trp Val Pro Val Ile Asn Leu Pro Glu
67               150               155               160
68   cgg tga tggcatctga atgaaaataa ctgaaccaa ttgcactgaa gtttttgaaa   831
69   Arg
70   165
71   tacctttgta gttactcaag cagttactcc ctacactgat gcaaggatta cagaaactga 891
72   tgccaagggg ctgagtgagt tcaactacat gttctggggg cccggagata gatgactttg 951
73   cagatggaaa gaggtgaaaa tgaagaagga agctgtgttg aaacagaaaa ataagtcaaa 1011
74   aggaacaaaa attacaaaga accatgcagg aaggaaaact atgtattaat ttagaatggg 1071
75   tgagttacat taaaataaac caaatatgtt aaagtttaag tgtgcagcca tagtttgggg 1131
76   atttttgggt tatatgccct caagtaaaag aaaagccgaa agggttaatc atatttgaaa 1191
77   accatatttt attgtatttt gatgagatat taaattctca aagttttatt ataaattcta 1251
78   ctaagttatt ttatgacatg aaaagttatt tatgtctataa attttttgaa acacaatacc 1311
79   tacaataaac tgggtatgaat aattgcatca tt                               1343
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 165
83 <212> TYPE: PRT
84 <213> ORGANISM: Homo sapiens
85 <400> SEQUENCE: 2
86   Met Thr Leu Glu Glu Phe Ser Ala Gly Glu Gln Lys Thr Glu Arg Met
87       1             5             10             15
88   Asp Lys Val Gly Asp Ala Leu Glu Glu Val Leu Ser Lys Ala Leu Ser
89               20             25             30
90   Gln Arg Thr Ile Thr Val Gly Val Tyr Glu Ala Ala Lys Leu Leu Asn
91               35             40             45
92   Val Asp Pro Asp Asn Val Val Leu Cys Leu Leu Ala Ala Asp Glu Asp
93               50             55             60
94   Asp Asp Arg Asp Val Ala Leu Gln Ile His Phe Thr Leu Ile Gln Ala

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95      65      70      75      80
96      Phe Cys Cys Glu Asn Asp Ile Asn Ile Leu Arg Val Ser Asn Pro Gly
97      85      90      95
98      Arg Leu Ala Glu Leu Leu Leu Glu Thr Asp Ala Gly Pro Ala Ala
99      100      105      110
100     Ser Glu Gly Ala Glu Gln Pro Pro Asp Leu His Cys Val Leu Val Thr
101     115      120      125
102     Asn Pro His Ser Ser Gln Trp Lys Asp Pro Ala Leu Ser Gln Leu Ile
103     130      135      140
104     Cys Phe Cys Arg Glu Ser Arg Tyr Met Asp Gln Trp Val Pro Val Ile
105     145      150      155      160
106     Asn Leu Pro Glu Arg
107     165
109 <210> SEQ ID NO: 3
110 <211> LENGTH: 31
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
115     amplification primer
116 <400> SEQUENCE: 3
117     ggcggctcga gactttggag gaattctcgg c 31
119 <210> SEQ ID NO: 4
120 <211> LENGTH: 24
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
125     amplification primer
126 <400> SEQUENCE: 4
127     catcaccggtt caggagatt aatc 24
129 <210> SEQ ID NO: 5
130 <211> LENGTH: 6
131 <212> TYPE: PRT
132 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Description of Artificial Sequence:GADD45
135     subsequence acidic motif amino acid residues
136     62-67; exemplary peptide inhibiting GADD45-related
137     dissociation of Cdc2/cyclin B1 complexes
138 <400> SEQUENCE: 5
139     Asp Glu Asp Asp Asp Arg
140     1      5
142 <210> SEQ ID NO: 6
143 <211> LENGTH: 160
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
146 <220> FEATURE:
147 <223> OTHER INFORMATION: human growth arrest and DNA-damage-inducible

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148     protein (hGADD45beta)
149 <400> SEQUENCE: 6
150     Met Thr Leu Glu Glu Leu Val Ala Cys Asp Asn Ala Ala Gln Lys Met
151         1             5             10             15
152     Gln Thr Val Thr Ala Ala Val Glu Glu Leu Leu Val Ala Ala Gln Arg
153         20             25             30
154     Gln Asp Arg Leu Thr Val Gly Val Tyr Glu Ser Ala Lys Leu Met Asn
155         35             40             45
156     Val Asp Pro Asp Ser Val Val Leu Cys Leu Leu Ala Ile Asp Glu Glu
157         50             55             60
158     Glu Glu Asp Asp Ile Ala Leu Gln Ile His Phe Thr Leu Ile Gln Ser
159         65             70             75             80
160     Phe Cys Cys Asp Asn Asp Ile Asn Ile Val Arg Val Ser Gly Met Gln
161         85             90             95
162     Arg Leu Ala Gln Leu Leu Gly Glu Pro Ala Glu Thr Gln Gly Thr Thr
163         100            105            110
164     Glu Ala Arg Asp Leu His Cys Leu Leu Val Thr Asn Pro His Thr Asp
165         115            120            125
166     Ala Trp Lys Ser His Gly Leu Val Glu Val Ala Ser Tyr Cys Glu Glu
167         130            135            140
168     Ser Arg Gly Asn Asn Gln Trp Val Pro Tyr Ile Ser Leu Gln Glu Arg
169         145            150            155            160
171 <210> SEQ ID NO: 7
172 <211> LENGTH: 159
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapiens
175 <220> FEATURE:
176 <223> OTHER INFORMATION: human growth arrest and DNA-damage-inducible
177     protein (hGADD45gamma)
178 <400> SEQUENCE: 7
179     Met Thr Leu Glu Glu Val Arg Gly Gln Asp Thr Val Pro Glu Ser Thr
180         1             5             10             15
181     Ala Arg Met Gln Gly Ala Gly Lys Ala Leu His Glu Leu Leu Leu Ser
182         20             25             30
183     Ala Gln Arg Gln Gly Cys Leu Thr Ala Gly Val Tyr Glu Ser Ala Lys
184         35             40             45
185     Val Leu Asn Val Asp Pro Asp Asn Val Thr Phe Cys Val Leu Ala Ala
186         50             55             60
187     Gly Glu Glu Asp Glu Gly Asp Ile Ala Leu Gln Ile His Phe Thr Leu
188         65             70             75             80
189     Ile Gln Ala Phe Cys Cys Glu Asn Asp Ile Asp Ile Val Arg Val Gly
190         85             90             95
191     Asp Val Gln Arg Leu Ala Ala Ile Val Gly Ala Gly Glu Glu Ala Gly
192         100            105            110
193     Ala Pro Gly Asp Leu His Cys Ile Leu Ile Ser Asn Pro Asn Glu Asp
194         115            120            125
195     Ala Trp Lys Asp Pro Ala Leu Glu Lys Leu Ser Leu Phe Cys Glu Glu
196         130            135            140
197     Ser Arg Ser Val Asn Asp Trp Val Pro Ser Ile Thr Leu Pro Glu

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198      145      150      155
200 <210> SEQ ID NO: 8
201 <211> LENGTH: 165
202 <212> TYPE: PRT
203 <213> ORGANISM: Mus musculus
204 <220> FEATURE:
205 <223> OTHER INFORMATION: mouse growth arrest and DNA-damage-inducible
206      protein (mGADD45)
207 <400> SEQUENCE: 8
208      Met Thr Leu Glu Glu Phe Ser Ala Ala Glu Gln Lys Thr Glu Arg Met
209      1          5          10          15
210      Asp Thr Val Gly Asp Ala Leu Glu Glu Val Leu Ser Lys Ala Arg Ser
211      20          25          30
212      Gln Arg Thr Ile Thr Val Gly Val Tyr Glu Ala Ala Lys Leu Leu Asn
213      35          40          45
214      Val Asp Pro Asp Asn Val Val Leu Cys Leu Leu Ala Ala Asp Glu Asp
215      50          55          60
216      Asp Asp Arg Asp Val Ala Leu Gln Ile His Phe Thr Leu Ile Arg Ala
217      65          70          75          80
218      Phe Cys Cys Glu Asn Asp Ile Asn Ile Leu Arg Val Ser Asn Pro Gly
219      85          90          95
220      Arg Leu Ala Glu Leu Leu Leu Leu Glu Asn Asp Ala Gly Pro Ala Glu
221      100         105         110
222      Ser Gly Gly Ala Ala Gln Thr Pro Asp Leu His Cys Val Leu Val Thr
223      115         120         125
224      Asn Pro His Ser Ser Gln Trp Lys Asp Pro Ala Leu Ser Gln Leu Ile
225      130         135         140
226      Cys Phe Cys Arg Glu Ser Arg Tyr Met Asp Gln Trp Val Pro Val Ile
227      145         150         155         160
228      Asn Leu Pro Glu Arg
229      165
231 <210> SEQ ID NO: 9
232 <211> LENGTH: 165
233 <212> TYPE: PRT
234 <213> ORGANISM: Rattus norvegicus
235 <220> FEATURE:
236 <223> OTHER INFORMATION: rat growth arrest and DNA-damage-inducible protein
237      (rGADD45)
238 <400> SEQUENCE: 9
239      Met Thr Leu Glu Glu Phe Ser Ala Ala Glu Gln Lys Ile Glu Arg Met
240      1          5          10          15
241      Asp Thr Val Gly Asp Ala Leu Glu Glu Val Leu Ser Lys Ala Arg Ser
242      20          25          30
243      Gln Arg Thr Ile Thr Val Gly Val Tyr Glu Ala Ala Lys Leu Leu Asn
244      35          40          45
245      Val Asp Pro Asp Asn Val Val Leu Cys Leu Leu Ala Ala Asp Glu Asp
246      50          55          60
247      Asp Asp Arg Asp Val Ala Leu Gln Ile His Phe Thr Leu Ile Arg Ala
248      65          70          75          80

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